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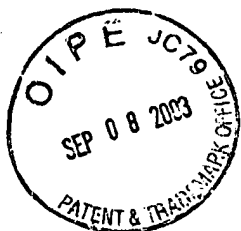
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SEQUENCE LISTING

<110> Steinaa, Lucilla
Mouritsen, Soren
Gautam, Anand
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Haaning, Jesper
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Nielsen, Klaus
Karlsson, Gunilla
Rasmussen, Peter

<120> Novel Methods for Therapeutic Vaccination

<130> 3631-0109P

<140> US 09/806,703

<141> 2001-04-04

<150> PCT/DK99/00525

<151> 1999-10-05

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<150> US 60/105,011

<151> 1998-10-20

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<170> PatentIn Ver. 3.0

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gct	gcc	ggc	tgc	acg	ggc	ccc	aag	cac	tct	gac	tgc	ctg	gcc	tgc	ctc	768
Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys	Leu	
		220				225						230				
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His	Phe	Asn	His	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro	Ala	Leu	Val	
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Thr	Tyr	Asn	Thr	Asp	Thr	Phe	Glu	Ser	Met	Pro	Asn	Pro	Glu	Gly	Arg	
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Tyr	Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Ala	Cys	Pro	Tyr	Asn	Tyr	Leu	
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Ser	Thr	Asp	Val	Gly	Ser	Cys	Thr	Leu	Val	Cys	Pro	Leu	His	Asn	Gln	
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gag	gtg	aca	gca	gag	gat	gga	aca	cag	cgg	tgt	gag	aag	tgc	agc	aag	1008
Glu	Val	Thr	Ala	Glu	Asp	Gly	Thr	Gln	Arg	Cys	Glu	Lys	Cys	Ser	Lys	
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ccc	tgt	gcc	cga	gtg	tgc	tat	ggc	ctg	ggc	atg	gag	cac	ttg	cga	gag	1056
Pro	Cys	Ala	Arg	Val	Cys	Tyr	Gly	Leu	Gly	Met	Glu	His	Leu	Arg	Glu	
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gtg	agg	gca	gtt	acc	agt	gcc	aat	atc	cag	gag	ttt	gct	ggc	tgc	aag	1104
Val	Arg	Ala	Val	Thr	Ser	Ala	Asn	Ile	Gln	Glu	Phe	Ala	Gly	Cys	Lys	
				335						340					345	
aag	atc	ttt	ggg	agc	ctg	gca	ttt	ctg	ccg	gag	agc	ttt	gat	ggg	gac	1152
Lys	Ile	Phe	Gly	Ser	Leu	Ala	Phe	Leu	Pro	Glu	Ser	Phe	Asp	Gly	Asp	
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Pro	Ala	Ser	Asn	Thr	Ala	Pro	Leu	Gln	Pro	Glu	Gln	Leu	Gln	Val	Phe	
			365					370					375			
gag	act	ctg	gaa	gag	atc	aca	ggc	tac	cta	tac	atc	tca	gca	tgg	ccg	1248
Glu	Thr	Leu	Glu	Glu	Ile	Thr	Gly	Tyr	Leu	Tyr	Ile	Ser	Ala	Trp	Pro	
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gac	agc	ctg	cct	gac	ctc	agc	gtc	ttc	cag	aac	ctg	caa	gta	atc	cgg	1296
Asp	Ser	Leu	Pro	Asp	Leu	Ser	Val	Phe	Gln	Asn	Leu	Gln	Val	Ile	Arg	
		395				400					405					
gga	cga	att	ctg	cac	aat	ggc	gcc	tac	tcg	ctg	acc	ctg	caa	ggg	ctg	1344
Gly	Arg	Ile	Leu	His	Asn	Gly	Ala	Tyr	Ser	Leu	Thr	Leu	Gln	Gly	Leu	
				415						420					425	
ggc	atc	agc	tgg	ctg	ggg	ctg	cgc	tca	ctg	agg	gaa	ctg	ggc	agt	gga	1392
Gly	Ile	Ser	Trp	Leu	Gly	Leu	Arg	Ser	Leu	Arg	Glu	Leu	Gly	Ser	Gly	
			430						435					440		
ctg	gcc	ctc	atc	cac	cat	aac	acc	cac	ctc	tgc	ttc	gtg	cac	acg	gtg	1440
Leu	Ala	Leu	Ile	His	His	Asn	Thr	His	Leu	Cys	Phe	Val	His	Thr	Val	
			445					450					455			
ccc	tgg	gac	cag	ctc	ttt	cgg	aac	ccg	cac	caa	gct	ctg	ctc	cac	act	1488

Pro	Trp	Asp	Gln	Leu	Phe	Arg	Asn	Pro	His	Gln	Ala	Leu	Leu	His	Thr	
		460					465					470				
gcc	aac	cgg	cca	gag	gac	gag	tgt	gtg	ggc	gag	ggc	ctg	gcc	tgc	cac	1536
Ala	Asn	Arg	Pro	Glu	Asp	Glu	Cys	Val	Gly	Glu	Gly	Leu	Ala	Cys	His	
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cag	ctg	tgc	gcc	cga	ggg	cac	tgc	tgg	ggc	cca	ggg	ccc	acc	cag	tgt	1584
Gln	Leu	Cys	Ala	Arg	Gly	His	Cys	Trp	Gly	Pro	Gly	Pro	Thr	Gln	Cys	
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Val	Asn	Cys	Ser	Gln	Phe	Leu	Arg	Gly	Gln	Glu	Cys	Val	Glu	Glu	Cys	
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Arg	Val	Leu	Gln	Gly	Leu	Pro	Arg	Glu	Tyr	Val	Asn	Ala	Arg	His	Cys	
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Phe	Gly	Pro	Glu	Ala	Asp	Gln	Cys	Val	Ala	Cys	Ala	His	Tyr	Lys	Asp	
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Pro	Pro	Phe	Cys	Val	Ala	Arg	Cys	Pro	Ser	Gly	Val	Lys	Pro	Asp	Leu	
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Ser	Tyr	Met	Pro	Ile	Trp	Lys	Phe	Pro	Asp	Glu	Glu	Gly	Ala	Cys	Gln	
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Pro	Cys	Pro	Ile	Asn	Cys	Thr	His	Ser	Cys	Val	Asp	Leu	Asp	Asp	Lys	
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aga	ctg	ctg	cag	gaa	acg	gag	ctg	gtg	gag	ccg	ctg	aca	cct	agc	gga	2112
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Ala	Met	Pro	Asn	Gln	Ala	Gln	Met	Arg	Ile	Leu	Lys	Glu	Thr	Glu	Leu	
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agg	aag	gtg	aag	gtg	ctt	gga	tct	ggc	gct	ttt	ggc	aca	gtc	tac	aag	2208
Arg	Lys	Val	Lys	Val	Leu	Gly	Ser	Gly	Ala	Phe	Gly	Thr	Val	Tyr	Lys	
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	810				815					820					825	
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ccc	atc	tgc	acc	att	gat	gtc	tac	atg	atc	atg	gtc	aaa	tgt	tgg	atg	2880
Pro	Ile	Cys	Thr	Ile	Asp	Val	Tyr	Met	Ile	Met	Val	Lys	Cys	Trp	Met	
			925					930					935			
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Ile	Asp	Ser	Glu	Cys	Arg	Pro	Arg	Phe	Arg	Glu	Leu	Val	Ser	Glu	Phe	
			940				945					950				
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Ser	Arg	Met	Ala	Arg	Asp	Pro	Gln	Arg	Phe	Val	Val	Ile	Gln	Asn	Glu	
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gta	ccc	cag	cag	ggc	ttc	ttc	tgt	cca	gac	cct	gcc	ccg	ggc	gct	ggg	3120
Val	Pro	Gln	Gln	Gly	Phe	Phe	Cys	Pro	Asp	Pro	Ala	Pro	Gly	Ala	Gly	
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Ser	Pro	Leu	Ala	Pro	Ser	Glu	Gly	Ala	Gly	Ser	Asp	Val	Phe	Asp	Gly	
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Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Val Pro Leu	
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Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu Thr Cys Ser Pro Gln	
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Arg Ala Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val	
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ttt gcc ttt ggg ggt gcc gtg gag aac ccc gag tac ttg aca ccc cag	3600
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Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala	
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Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala	
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cca ccc agc acc ttc aaa ggg aca cct acg gca gag aac cca gag tac	3744
Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu Tyr	
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Leu Gly Leu Asp Val Pro Val	
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 -5 -1 1 5
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 Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
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 Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
 45 50 55
 Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu
 60 65 70
 Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
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 Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro
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Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu	Gln	Leu	Arg	Ser	110	115	120
Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg	Asn	Pro	Gln	125	130	135
Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe	His	Lys	Asn	140	145	150
Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala	Cys	155	160	165
His	Pro	Cys	Ser	Pro	Met	Cys	Lys	Gly	Ser	Arg	Cys	Trp	Gly	Glu	Ser	170	175	180
Ser	Glu	Asp	Cys	Gln	Ser	Leu	Thr	Arg	Thr	Val	Cys	Ala	Gly	Gly	Cys	190	195	200
Ala	Arg	Cys	Lys	Gly	Pro	Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln	Cys	205	210	215
Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys	Leu	220	225	230
His	Phe	Asn	His	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro	Ala	Leu	Val	235	240	245
Thr	Tyr	Asn	Thr	Asp	Thr	Phe	Glu	Ser	Met	Pro	Asn	Pro	Glu	Gly	Arg	250	255	260
Tyr	Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Ala	Cys	Pro	Tyr	Asn	Tyr	Leu	270	275	280
Ser	Thr	Asp	Val	Gly	Ser	Cys	Thr	Leu	Val	Cys	Pro	Leu	His	Asn	Gln	285	290	295
Glu	Val	Thr	Ala	Glu	Asp	Gly	Thr	Gln	Arg	Cys	Glu	Lys	Cys	Ser	Lys	300	305	310
Pro	Cys	Ala	Arg	Val	Cys	Tyr	Gly	Leu	Gly	Met	Glu	His	Leu	Arg	Glu	315	320	325
Val	Arg	Ala	Val	Thr	Ser	Ala	Asn	Ile	Gln	Glu	Phe	Ala	Gly	Cys	Lys	330	335	340
Lys	Ile	Phe	Gly	Ser	Leu	Ala	Phe	Leu	Pro	Glu	Ser	Phe	Asp	Gly	Asp	350	355	360
Pro	Ala	Ser	Asn	Thr	Ala	Pro	Leu	Gln	Pro	Glu	Gln	Leu	Gln	Val	Phe	365	370	375
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Asp	Ser	Leu	Pro	Asp	Leu	Ser	Val	Phe	Gln	Asn	Leu	Gln	Val	Ile	Arg	395	400	405
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Gly	Ile	Ser	Trp	Leu	Gly	Leu	Arg	Ser	Leu	Arg	Glu	Leu	Gly	Ser	Gly	430	435	440
Leu	Ala	Leu	Ile	His	His	Asn	Thr	His	Leu	Cys	Phe	Val	His	Thr	Val	445	450	455
Pro	Trp	Asp	Gln	Leu	Phe	Arg	Asn	Pro	His	Gln	Ala	Leu	Leu	His	Thr	460	465	470
Ala	Asn	Arg	Pro	Glu	Asp	Glu	Cys	Val	Gly	Glu	Gly	Leu	Ala	Cys	His	475	480	485
Gln	Leu	Cys	Ala	Arg	Gly	His	Cys	Trp	Gly	Pro	Gly	Pro	Thr	Gln	Cys	490	495	500
Val	Asn	Cys	Ser	Gln	Phe	Leu	Arg	Gly	Gln	Glu	Cys	Val	Glu	Glu	Cys	510	515	520
Arg	Val	Leu	Gln	Gly	Leu	Pro	Arg	Glu	Tyr	Val	Asn	Ala	Arg	His	Cys	525	530	535
Leu	Pro	Cys	His	Pro	Glu	Cys	Gln	Pro	Gln	Asn	Gly	Ser	Val	Thr	Cys	540	545	550
Phe	Gly	Pro	Glu	Ala	Asp	Gln	Cys	Val	Ala	Cys	Ala	His	Tyr	Lys	Asp			

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Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln		585
	590	595
Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys		600
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Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser Ile Val Ser		615
	620	625
Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly		630
	635	640
Ile Leu Ile Lys Arg Arg Gln Gln Lys Ile Arg Lys Tyr Thr Met Arg		645
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Arg Leu Leu Gln Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly		665
	670	675
Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu		680
	685	690
Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys		695
	700	705
Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile		710
	715	720
Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu		725
730	735	740
Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg		745
	750	755
Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln Leu		760
	765	770
Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu Asn Arg Gly Arg		775
	780	785
Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala Lys Gly		790
	795	800
Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala		805
810	815	820
Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe		825
	830	835
Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp		840
	845	850
Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg		855
	860	865
Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val		870
	875	880
Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro Ala		885
890	895	900
Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro		905
	910	915
Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met		920
	925	930
Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu Phe		935
	940	945
Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn Glu		950
	955	960
Asp Leu Gly Pro Ala Ser Pro Leu Asp Ser Thr Phe Tyr Arg Ser Leu		965
970	975	980
Leu Glu Asp Asp Asp Met Gly Asp Leu Val Asp Ala Glu Glu Tyr Leu		985
	990	995
Val Pro Gln Gln Gly Phe Phe Cys Pro Asp Pro Ala Pro Gly Ala Gly		1000
	1005	1010
		1015

Gly Met Val His His Arg His Arg Ser Ser Ser Thr Arg Ser Gly Gly
 1020 1025 1030
 Gly Asp Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Glu Ala Pro Arg
 1035 1040 1045
 Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly Ser Asp Val Phe Asp Gly
 1050 1055 1060 1065
 Asp Leu Gly Met Gly Ala Ala Lys Gly Leu Gln Ser Leu Pro Thr His
 1070 1075 1080
 Asp Pro Ser Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Val Pro Leu
 1085 1090 1095
 Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu Thr Cys Ser Pro Gln
 1100 1105 1110
 Pro Glu Tyr Val Asn Gln Pro Asp Val Arg Pro Gln Pro Pro Ser Pro
 1115 1120 1125
 Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu
 1130 1135 1140 1145
 Arg Ala Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val
 1150 1155 1160
 Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln
 1165 1170 1175
 Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala
 1180 1185 1190
 Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala
 1195 1200 1205
 Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu Tyr
 1210 1215 1220 1225
 Leu Gly Leu Asp Val Pro Val
 1230

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 <211> 648
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)..(648)

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 Met Gly Ser Pro Arg Ser Ala Leu Ser Cys Leu Leu Leu His Leu Leu
 1 5 10 15
 gtt ctc tgc ctc caa gcc cag gta act gtt cag tcc tca cct aat ttt 96
 Val Leu Cys Leu Gln Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe
 20 25 30
 aca cag cat gtg agg gag cag agc ctg gtg acg gat cag ctc agc cgc 144
 Thr Gln His Val Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg
 35 40 45
 cgc ctc atc cgg acc tac cag ctc tac agc cgc acc agc ggg aag cac 192
 Arg Leu Ile Arg Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His
 50 55 60
 gtg cag gtc ctg gcc aac aag cgc atc aac gcc atg gca gaa gac gga 240
 Val Gln Val Leu Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly
 65 70 75 80
 gac ccc ttc gcg aag ctc att gtg gag acc gat act ttt gga agc aga 288
 Asp Pro Phe Ala Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg

	85	90	95	
gtc cga gtt cgc ggc gca gag aca ggt ctc tac atc tgc atg aac aag				336
Val Arg Val Arg Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys				
	100	105	110	
aag ggg aag cta att gcc aag agc aac ggc aaa ggc aag gac tgc gta				384
Lys Gly Lys Leu Ile Ala Lys Ser Asn Gly Lys Gly Lys Asp Cys Val				
	115	120	125	
ttc aca gag atc gtg ctg gag aac aac tac acg gcg ctg cag aac gcc				432
Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala				
	130	135	140	
aag tac gag ggc tgg tac atg gcc ttt acc cgc aag ggc cgg ccc cgc				480
Lys Tyr Glu Gly Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg				
	145	150	155	160
aag ggc tcc aag acg cgc cag cat cag cgc gag gtg cac ttc atg aag				528
Lys Gly Ser Lys Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys				
	165	170	175	
cgc ctg ccg cgg ggc cac cac acc acc gag cag agc ctg cgc ttc gag				576
Arg Leu Pro Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu				
	180	185	190	
ttc ctc aac tac ccg ccc ttc acg cgc agc ctg cgc ggc agc cag agg				624
Phe Leu Asn Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg				
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act tgg gcc ccg gag ccc cga tag				648
Thr Trp Ala Pro Glu Pro Arg				
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<211> 215

<212> PRT

<213> Homo sapiens

<400> 6

Met Gly Ser Pro Arg Ser Ala Leu Ser Cys Leu Leu Leu His Leu Leu				
1 5 10 15				
Val Leu Cys Leu Gln Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe				
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Thr Gln His Val Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg				
35 40 45				
Arg Leu Ile Arg Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His				
50 55 60				
Val Gln Val Leu Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly				
65 70 75 80				
Asp Pro Phe Ala Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg				
85 90 95				
Val Arg Val Arg Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys				
100 105 110				
Lys Gly Lys Leu Ile Ala Lys Ser Asn Gly Lys Gly Lys Asp Cys Val				
115 120 125				
Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala				
130 135 140				
Lys Tyr Glu Gly Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg				
145 150 155 160				
Lys Gly Ser Lys Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys				
165 170 175				
Arg Leu Pro Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu				
180 185 190				

Phe Leu Asn Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg
 195 200 205
 Thr Trp Ala Pro Glu Pro Arg
 210 215

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 <212> DNA
 <213> Mus musculus

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 <222> (1)..(2256)

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 1 5 10 15
 cgc cag cgc tgg ctc cgt gtt ggg aca ctg gtg ctg gct tta acc gga 96
 Arg Gln Arg Trp Leu Arg Val Gly Thr Leu Val Leu Ala Leu Thr Gly
 20 25 30
 acc ttc ctc att ggc ttc ctc ttt ggg tgg ttt ata aaa cct tcc aat 144
 Thr Phe Leu Ile Gly Phe Leu Phe Gly Trp Phe Ile Lys Pro Ser Asn
 35 40 45
 gaa gct act ggt aat gtt tcc cat tct ggc atg aag aag gag ttt ttg 192
 Glu Ala Thr Gly Asn Val Ser His Ser Gly Met Lys Lys Glu Phe Leu
 50 55 60
 cat gaa ttg aag gct gag aac atc aaa aaa ttt tta tac aat ttc aca 240
 His Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr
 65 70 75 80
 cgg aca cca cac ttg gca gga aca caa aat aat ttt gag ctt gca aag 288
 Arg Thr Pro His Leu Ala Gly Thr Gln Asn Asn Phe Glu Leu Ala Lys
 85 90 95
 caa att cat gac cag tgg aaa gaa ttt ggc ctg gat ttg gtt gag tta 336
 Gln Ile His Asp Gln Trp Lys Glu Phe Gly Leu Asp Leu Val Glu Leu
 100 105 110
 tcc cat tac gat gtc ttg ctg tcc tat cca aat aaa act cat cct aac 384
 Ser His Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn
 115 120 125
 tat atc tca ata att aat gaa gat gga aat gag att ttc aaa aca tca 432
 Tyr Ile Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Lys Thr Ser
 130 135 140
 tta tct gaa cag cca ccc cca gga tat gag aat ata tca gat gta gtg 480
 Leu Ser Glu Gln Pro Pro Pro Gly Tyr Glu Asn Ile Ser Asp Val Val
 145 150 155 160
 cca cca tac agt gcc ttc tct cca caa ggg aca cca gag ggt gat cta 528
 Pro Pro Tyr Ser Ala Phe Ser Pro Gln Gly Thr Pro Glu Gly Asp Leu
 165 170 175
 gtg tat gtc aac tat gca cga act gaa gac ttc ttt aaa ctg gaa cgg 576
 Val Tyr Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg
 180 185 190
 gaa atg aag atc agt tgt tct ggg aag att gtg att gcc aga tat ggg 624
 Glu Met Lys Ile Ser Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly
 195 200 205
 aaa gtg ttc aga gga aat atg gtt aaa aat gct caa ctg gca ggg gca 672

Lys	Val	Phe	Arg	Gly	Asn	Met	Val	Lys	Asn	Ala	Gln	Leu	Ala	Gly	Ala		
210						215					220						
aaa	gga	atg	att	ctg	tac	tca	gac	cct	gct	gac	tac	ttt	gtt	cct	gcg	720	
Lys	Gly	Met	Ile	Leu	Tyr	Ser	Asp	Pro	Ala	Asp	Tyr	Phe	Val	Pro	Ala		
225					230					235					240		
gtg	aag	tcc	tat	cca	gat	ggc	tgg	aac	ctc	cct	gga	ggg	ggg	gtc	caa	763	
Val	Lys	Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu	Pro	Gly	Gly	Gly	Val	Gln		
				245				250						255			
cgt	gga	aat	gtc	tta	aat	ctt	aat	ggg	gca	ggg	gac	ccg	ctc	aca	cca	816	
Arg	Gly	Asn	Val	Leu	Asn	Leu	Asn	Gly	Ala	Gly	Asp	Pro	Leu	Thr	Pro		
			260					265					270				
ggg	tac	cca	gca	aat	gaa	cat	gct	tat	agg	cat	gag	ttg	aca	aac	gct	864	
Gly	Tyr	Pro	Ala	Asn	Glu	His	Ala	Tyr	Arg	His	Glu	Leu	Thr	Asn	Ala		
		275					280					285					
gtt	ggc	ctt	cca	agt	att	cct	gtc	cat	cct	att	gga	tat	gat	gat	gca	912	
Val	Gly	Leu	Pro	Ser	Ile	Pro	Val	His	Pro	Ile	Gly	Tyr	Asp	Asp	Ala		
	290					295					300						
cag	aaa	ctc	tta	gaa	cac	atg	ggg	ggg	cca	gca	ccc	cct	gac	agt	agc	960	
Gln	Lys	Leu	Leu	Glu	His	Met	Gly	Gly	Pro	Ala	Pro	Pro	Asp	Ser	Ser		
305					310				315						320		
tgg	aag	gga	gga	tta	aaa	gtg	cct	tac	aac	gtg	gga	cct	ggc	ttt	gct	1008	
Trp	Lys	Gly	Gly	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly	Pro	Gly	Phe	Ala		
				325					330					335			
gga	aac	ttt	tca	aca	caa	aag	gtc	aag	atg	cat	att	cac	tct	tac	act	1056	
Gly	Asn	Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His	Ile	His	Ser	Tyr	Thr		
		340						345				350					
aaa	gtg	aca	aga	atc	tat	aat	gtc	att	ggc	acc	ctc	aaa	gga	gct	ctg	1104	
Lys	Val	Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly	Thr	Leu	Lys	Gly	Ala	Leu		
		355					360					365					
gaa	cca	gac	aga	tat	gtt	att	ctt	gga	ggg	cac	cga	gac	gct	tgg	gta	1152	
Glu	Pro	Asp	Arg	Tyr	Val	Ile	Leu	Gly	Gly	His	Arg	Asp	Ala	Trp	Val		
	370					375					380						
ttt	ggg	ggc	att	gac	cct	cag	agt	gga	gca	gct	gtt	gtt	cat	gaa	att	1200	
Phe	Gly	Gly	Ile	Asp	Pro	Gln	Ser	Gly	Ala	Ala	Val	Val	His	Glu	Ile		
385					390					395					400		
gtg	cgg	agc	ttt	gga	acc	ctg	aag	aag	aaa	gga	cgg	agg	cct	aga	agg	1248	
Val	Arg	Ser	Phe	Gly	Thr	Leu	Lys	Lys	Lys	Gly	Arg	Arg	Pro	Arg	Arg		
				405				410					415				
aca	att	ttg	ttt	gca	agc	tgg	gat	gca	gaa	gaa	ttt	ggc	ctt	ctt	ggg	1296	
Thr	Ile	Leu	Phe	Ala	Ser	Trp	Asp	Ala	Glu	Glu	Phe	Gly	Leu	Leu	Gly		
			420					425					430				
tct	act	gag	tgg	gca	gag	gaa	cat	tca	aga	ctc	cta	caa	gag	cga	ggg	1344	
Ser	Thr	Glu	Trp	Ala	Glu	Glu	His	Ser	Arg	Leu	Leu	Gln	Glu	Arg	Gly		
		435					440					445					
gtg	gct	tat	att	aat	gct	gat	tct	tcc	ata	gaa	gga	aat	tac	act	cta	1392	
Val	Ala	Tyr	Ile	Asn	Ala	Asp	Ser	Ser	Ile	Glu	Gly	Asn	Tyr	Thr	Leu		
	450					455					460						
aga	gtt	gat	tgc	aca	cca	ctg	atg	tac	agc	tta	gtg	tac	aac	cta	aca	1440	
Arg	Val	Asp	Cys	Thr	Pro	Leu	Met	Tyr	Ser	Leu	Val	Tyr	Asn	Leu	Thr		
465					470					475					480		
aaa	gag	ctg	caa	agc	cca	gat	gaa	ggg	ttt	gaa	gga	aaa	tct	ctt	tat	1488	
Lys	Glu	Leu	Gln	Ser	Pro	Asp	Glu	Gly	Phe	Glu	Gly	Lys	Ser	Leu	Tyr		
				485				490						495			
gac	agc	tgg	aaa	gaa	aag	agt	cct	tca	cct	gag	ttc	att	gga	atg	ccc	1536	
Asp	Ser	Trp	Lys	Glu	Lys	Ser	Pro	Ser	Pro	Glu	Phe	Ile	Gly	Met	Pro		
			500				505					510					
aga	att	agc	aag	ctg	ggg	tct	ggc	aat	gat	ttt	gaa	gtg	ttc	ttc	caa	1584	

Arg	Ile	Ser	Lys	Leu	Gly	Ser	Gly	Asn	Asp	Phe	Glu	Val	Phe	Phe	Gln		
		515					520					525					
aga	ctt	gga	att	gct	tca	ggc	aga	gcc	cga	tat	act	aaa	aat	tgg	aaa	1632	
Arg	Leu	Gly	Ile	Ala	Ser	Gly	Arg	Ala	Arg	Tyr	Thr	Lys	Asn	Trp	Lys		
	530					535					540						
act	aac	aaa	gtc	agc	agc	tat	cct	ctc	tat	cac	agt	gtc	tat	gaa	aca	1680	
Thr	Asn	Lys	Val	Ser	Ser	Tyr	Pro	Leu	Tyr	His	Ser	Val	Tyr	Glu	Thr		
	545				550					555					560		
tat	gag	ctg	gta	gta	aaa	ttt	tat	gac	cca	aca	ttt	aaa	tac	cac	ctc	1728	
Tyr	Glu	Leu	Val	Val	Lys	Phe	Tyr	Asp	Pro	Thr	Phe	Lys	Tyr	His	Leu		
			565						570					575			
act	gtg	gcc	cag	gtt	cga	gga	gcg	atg	gta	ttt	gaa	ctt	gcc	aat	tct	1776	
Thr	Val	Ala	Gln	Val	Arg	Gly	Ala	Met	Val	Phe	Glu	Leu	Ala	Asn	Ser		
			580					585					590				
ata	gtg	ctt	ccc	ttt	gac	tgc	caa	agt	tat	gct	gta	gct	ctg	aag	aag	1824	
Ile	Val	Leu	Pro	Phe	Asp	Cys	Gln	Ser	Tyr	Ala	Val	Ala	Leu	Lys	Lys		
			595				600						605				
tat	gct	gac	act	atc	tac	aat	att	tca	atg	aaa	cat	cca	caa	gaa	atg	1872	
Tyr	Ala	Asp	Thr	Ile	Tyr	Asn	Ile	Ser	Met	Lys	His	Pro	Gln	Glu	Met		
	610					615					620						
aag	gct	tac	atg	ata	tca	ttt	gat	tca	ctg	ttt	tct	gca	gtc	aat	aat	1920	
Lys	Ala	Tyr	Met	Ile	Ser	Phe	Asp	Ser	Leu	Phe	Ser	Ala	Val	Asn	Asn		
	625					630				635					640		
ttt	aca	gat	gtt	gca	tct	aag	ttc	aat	cag	aga	ctg	caa	gag	tta	gac	1968	
Phe	Thr	Asp	Val	Ala	Ser	Lys	Phe	Asn	Gln	Arg	Leu	Gln	Glu	Leu	Asp		
			645						650					655			
aaa	agc	aac	ccc	ata	tta	ctg	aga	att	atg	aat	gac	cag	ctg	atg	tat	2016	
Lys	Ser	Asn	Pro	Ile	Leu	Leu	Arg	Ile	Met	Asn	Asp	Gln	Leu	Met	Tyr		
			660					665					670				
ctg	gaa	cgt	gca	ttc	att	gat	cct	tta	ggc	tta	cca	gga	agg	cct	ttc	2064	
Leu	Glu	Arg	Ala	Phe	Ile	Asp	Pro	Leu	Gly	Leu	Pro	Gly	Arg	Pro	Phe		
			675				680					685					
tac	agg	cat	acc	atc	tat	gct	cca	agc	agc	cac	aac	aag	tat	gca	gga	2112	
Tyr	Arg	His	Thr	Ile	Tyr	Ala	Pro	Ser	Ser	His	Asn	Lys	Tyr	Ala	Gly		
			690			695					700						
gaa	tca	ttc	cct	ggg	att	tat	gat	gcc	ctt	ttt	gat	ata	agt	agc	aaa	2160	
Glu	Ser	Phe	Pro	Gly	Ile	Tyr	Asp	Ala	Leu	Phe	Asp	Ile	Ser	Ser	Lys		
			705		710				715						720		
gtc	aat	gct	tct	aag	gcc	tgg	aac	gaa	gtg	aag	aga	cag	att	tct	att	2208	
Val	Asn	Ala	Ser	Lys	Ala	Trp	Asn	Glu	Val	Lys	Arg	Gln	Ile	Ser	Ile		
			725					730						735			
gca	acc	ttt	aca	gtg	caa	gct	gca	gca	gag	act	ctg	agg	gaa	gta	gct	2256	
Ala	Thr	Phe	Thr	Val	Gln	Ala	Ala	Ala	Glu	Thr	Leu	Arg	Glu	Val	Ala		
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<211> 752

<212> PRT

<213> Mus musculus

<400> 8

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Arg	Gln	Arg	Trp	Leu	Arg	Val	Gly	Thr	Leu	Val	Leu	Ala	Leu	Thr	Gly		
			20				25						30				
Thr	Phe	Leu	Ile	Gly	Phe	Leu	Phe	Gly	Trp	Phe	Ile	Lys	Pro	Ser	Asn		

Asp	Ser	Trp	Lys	Glu	Lys	Ser	Pro	Ser	Pro	Glu	Phe	Ile	Gly	Met	Pro
			500					505					510		
Arg	Ile	Ser	Lys	Leu	Gly	Ser	Gly	Asn	Asp	Phe	Glu	Val	Phe	Phe	Gln
		515					520					525			
Arg	Leu	Gly	Ile	Ala	Ser	Gly	Arg	Ala	Arg	Tyr	Thr	Lys	Asn	Trp	Lys
	530					535					540				
Thr	Asn	Lys	Val	Ser	Ser	Tyr	Pro	Leu	Tyr	His	Ser	Val	Tyr	Glu	Thr
545					550					555					560
Tyr	Glu	Leu	Val	Val	Lys	Phe	Tyr	Asp	Pro	Thr	Phe	Lys	Tyr	His	Leu
			565						570					575	
Thr	Val	Ala	Gln	Val	Arg	Gly	Ala	Met	Val	Phe	Glu	Leu	Ala	Asn	Ser
			580					585					590		
Ile	Val	Leu	Pro	Phe	Asp	Cys	Gln	Ser	Tyr	Ala	Val	Ala	Leu	Lys	Lys
	595						600					605			
Tyr	Ala	Asp	Thr	Ile	Tyr	Asn	Ile	Ser	Met	Lys	His	Pro	Gln	Glu	Met
	610					615					620				
Lys	Ala	Tyr	Met	Ile	Ser	Phe	Asp	Ser	Leu	Phe	Ser	Ala	Val	Asn	Asn
625					630					635					640
Phe	Thr	Asp	Val	Ala	Ser	Lys	Phe	Asn	Gln	Arg	Leu	Gln	Glu	Leu	Asp
			645						650					655	
Lys	Ser	Asn	Pro	Ile	Leu	Leu	Arg	Ile	Met	Asn	Asp	Gln	Leu	Met	Tyr
		660						665					670		
Leu	Glu	Arg	Ala	Phe	Ile	Asp	Pro	Leu	Gly	Leu	Pro	Gly	Arg	Pro	Phe
	675						680					685			
Tyr	Arg	His	Thr	Ile	Tyr	Ala	Pro	Ser	Ser	His	Asn	Lys	Tyr	Ala	Gly
	690					695					700				
Glu	Ser	Phe	Pro	Gly	Ile	Tyr	Asp	Ala	Leu	Phe	Asp	Ile	Ser	Ser	Lys
705					710					715					720
Val	Asn	Ala	Ser	Lys	Ala	Trp	Asn	Glu	Val	Lys	Arg	Gln	Ile	Ser	Ile
			725						730					735	
Ala	Thr	Phe	Thr	Val	Gln	Ala	Ala	Ala	Glu	Thr	Leu	Arg	Glu	Val	Ala
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 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(2082)

<400> 9																
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Met	Lys	Lys	Glu	Phe	Leu	His	Glu	Leu	Lys	Ala	Glu	Asn	Ile	Lys	Lys	
1				5					10					15		
ttt	tta	tac	aat	ttc	aca	cgg	aca	cca	cac	ttg	gca	gga	aca	caa	aat	96
Phe	Leu	Tyr	Asn	Phe	Thr	Arg	Thr	Pro	His	Leu	Ala	Gly	Thr	Gln	Asn	
			20					25					30			
aat	ttt	gag	ctt	gca	aag	caa	att	cat	gac	cag	tg	aaa	gaa	ttt	ggc	144
Asn	Phe	Glu	Leu	Ala	Lys	Gln	Ile	His	Asp	Gln	Trp	Lys	Glu	Phe	Gly	
			35				40					45				
ctg	gat	ttg	gtt	gag	tta	tcc	cat	tac	gat	gtc	ttg	ctg	tcc	tat	cca	192
Leu	Asp	Leu	Val	Glu	Leu	Ser	His	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro	
	50					55					60					

aat	aaa	act	cat	cct	aac	tat	atc	tca	ata	ata	aat	gaa	gat	gga	aat	240
Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile	Ser	Ile	Ile	Asn	Glu	Asp	Gly	Asn	
65					70					75					80	
gag	att	ttc	aaa	aca	tca	tta	tct	gaa	cag	cca	ccc	cca	gga	tat	gag	288
Glu	Ile	Phe	Lys	Thr	Ser	Leu	Ser	Glu	Gln	Pro	Pro	Pro	Gly	Tyr	Glu	
				85				90						95		
aat	ata	tca	gat	gta	gtg	cca	cca	tac	agt	gcc	ttc	tct	cca	caa	ggg	336
Asn	Ile	Ser	Asp	Val	Val	Pro	Pro	Tyr	Ser	Ala	Phe	Ser	Pro	Gln	Gly	
			100					105					110			
aca	cca	gag	ggg	gat	cta	gtg	tat	gtc	aac	tat	gca	cga	act	gaa	gac	384
Thr	Pro	Glu	Gly	Asp	Leu	Val	Tyr	Val	Asn	Tyr	Ala	Arg	Thr	Glu	Asp	
	115					120						125				
ttc	ttt	aaa	ctg	gaa	cgg	gaa	atg	aag	atc	agt	tgt	tct	ggg	aag	att	432
Phe	Phe	Lys	Leu	Glu	Arg	Glu	Met	Lys	Ile	Ser	Cys	Ser	Gly	Lys	Ile	
130						135					140					
gtg	att	gcc	aga	tat	ggg	aaa	gtg	ttc	aga	gga	aat	atg	gtt	aaa	aat	480
Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val	Phe	Arg	Gly	Asn	Met	Val	Lys	Asn	
145					150					155					160	
gct	caa	ctg	gca	ggg	gca	aaa	gga	atg	att	ctg	tac	tca	gac	cct	gct	528
Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly	Met	Ile	Leu	Tyr	Ser	Asp	Pro	Ala	
				165				170						175		
gac	tac	ttt	gtt	cct	gcg	gtg	aag	tcc	tat	cca	gat	ggc	tgg	aac	ctc	576
Asp	Tyr	Phe	Val	Pro	Ala	Val	Lys	Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu	
			180					185					190			
cct	gga	ggg	ggg	gtc	caa	cgt	gga	aat	gtc	tta	aat	ctt	aat	ggg	gca	624
Pro	Gly	Gly	Gly	Val	Gln	Arg	Gly	Asn	Val	Leu	Asn	Leu	Asn	Gly	Ala	
	195					200						205				
ggg	gac	ccg	ctc	aca	cca	ggg	tac	cca	gca	aat	gaa	cat	gct	tat	agg	672
Gly	Asp	Pro	Leu	Thr	Pro	Gly	Tyr	Pro	Ala	Asn	Glu	His	Ala	Tyr	Arg	
	210					215					220					
cat	gag	ttg	aca	aac	gct	gtt	ggc	ctt	cca	agt	att	cct	gtc	cat	cct	720
His	Glu	Leu	Thr	Asn	Ala	Val	Gly	Leu	Pro	Ser	Ile	Pro	Val	His	Pro	
225					230					235					240	
att	gga	tat	gat	gat	gca	cag	aaa	ctc	tta	gaa	cac	atg	ggg	ggg	cca	768
Ile	Gly	Tyr	Asp	Asp	Ala	Gln	Lys	Leu	Leu	Glu	His	Met	Gly	Gly	Pro	
				245				250						255		
gca	ccc	cct	gac	agt	agc	tgg	aag	gga	gga	tta	aaa	gtg	cct	tac	aac	816
Ala	Pro	Pro	Asp	Ser	Ser	Trp	Lys	Gly	Gly	Leu	Lys	Val	Pro	Tyr	Asn	
			260					265					270			
gtg	gga	cct	ggc	ttt	gct	gga	aac	ttt	tca	aca	caa	aag	gtc	aag	atg	864
Val	Gly	Pro	Gly	Phe	Ala	Gly	Asn	Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	
	275					280						285				
cat	att	cac	tct	tac	act	aaa	gtg	aca	aga	atc	tat	aat	gtc	att	ggc	912
His	Ile	His	Ser	Tyr	Thr	Lys	Val	Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly	
	290					295					300					
acc	ctc	aaa	gga	gct	ctg	gaa	cca	gac	aga	tat	gtt	att	ctt	gga	ggg	960
Thr	Leu	Lys	Gly	Ala	Leu	Glu	Pro	Asp	Arg	Tyr	Val	Ile	Leu	Gly	Gly	
305					310					315					320	
cac	cga	gac	gct	tgg	gta	ttt	ggg	ggc	att	gac	cct	cag	agt	gga	gca	1008
His	Arg	Asp	Ala	Trp	Val	Phe	Gly	Gly	Ile	Asp	Pro	Gln	Ser	Gly	Ala	
				325				330						335		
gct	gtt	gtt	cat	gaa	att	gtg	cgg	agc	ttt	gga	acc	ctg	aag	aag	aaa	1056
Ala	Val	Val	His	Glu	Ile	Val	Arg	Ser	Phe	Gly	Thr	Leu	Lys	Lys	Lys	
			340					345					350			
gga	cgg	agg	cct	aga	agg	aca	att	ttg	ttt	gca	agc	tgg	gat	gca	gaa	1104
Gly	Arg	Arg	Pro	Arg	Arg	Thr	Ile	Leu	Phe	Ala	Ser	Trp	Asp	Ala	Glu	
	355					360						365				

gaa ttt ggc ctt ctt ggt tct act gag tgg gca gag gaa cat tca aga	1152
Glu Phe Gly Leu Leu Gly Ser Thr Glu Trp Ala Glu Glu His Ser Arg	
370 375 380	
ctc cta caa gag cga ggt gtg gct tat att aat gct gat tct tcc ata	1200
Leu Leu Gln Glu Arg Gly Val Ala Tyr Ile Asn Ala Asp Ser Ser Ile	
385 390 395 400	
gaa gga aat tac act cta aga gtt gat tgc aca cca ctg atg tac agc	1248
Glu Gly Asn Tyr Thr Leu Arg Val Asp Cys Thr Pro Leu Met Tyr Ser	
405 410 415	
tta gtg tac aac cta aca aaa gag ctg caa agc cca gat gaa ggt ttt	1296
Leu Val Tyr Asn Leu Thr Lys Glu Leu Gln Ser Pro Asp Glu Gly Phe	
420 425 430	
gaa gga aaa tct ctt tat gac agc tgg aaa gaa aag agt cct tca cct	1344
Glu Gly Lys Ser Leu Tyr Asp Ser Trp Lys Glu Lys Ser Pro Ser Pro	
435 440 445	
gag ttc att gga atg ccc aga att agc aag ctg ggg tct ggc aat gat	1392
Glu Phe Ile Gly Met Pro Arg Ile Ser Lys Leu Gly Ser Gly Asn Asp	
450 455 460	
ttt gaa gtg ttc ttc caa aga ctt gga att gct tca ggc aga gcc cga	1440
Phe Glu Val Phe Phe Gln Arg Leu Gly Ile Ala Ser Gly Arg Ala Arg	
465 470 475 480	
tat act aaa aat tgg aaa act aac aaa gtc agc agc tat cct ctc tat	1488
Tyr Thr Lys Asn Trp Lys Thr Asn Lys Val Ser Ser Tyr Pro Leu Tyr	
485 490 495	
cac agt gtc tat gaa aca tat gag ctg gta gta aaa ttt tat gac cca	1536
His Ser Val Tyr Glu Thr Tyr Glu Leu Val Val Lys Phe Tyr Asp Pro	
500 505 510	
aca ttt aaa tac cac ctc act gtg gcc cag gtt cga gga gcg atg gta	1584
Thr Phe Lys Tyr His Leu Thr Val Ala Gln Val Arg Gly Ala Met Val	
515 520 525	
ttt gaa ctt gcc aat tct ata gtg ctt ccc ttt gac tgc caa agt tat	1632
Phe Glu Leu Ala Asn Ser Ile Val Leu Pro Phe Asp Cys Gln Ser Tyr	
530 535 540	
gct gta gct ctg aag aag tat gct gac act atc tac aat att tca atg	1680
Ala Val Ala Leu Lys Lys Tyr Ala Asp Thr Ile Tyr Asn Ile Ser Met	
545 550 555 560	
aaa cat cca caa gaa atg aag gct tac atg ata tca ttt gat tca ctg	1728
Lys His Pro Gln Glu Met Lys Ala Tyr Met Ile Ser Phe Asp Ser Leu	
565 570 575	
ttt tct gca gtc aat aat ttt aca gat gtt gca tct aag ttc aat cag	1776
Phe Ser Ala Val Asn Asn Phe Thr Asp Val Ala Ser Lys Phe Asn Gln	
580 585 590	
aga ctg caa gag tta gac aaa agc aac ccc ata tta ctg aga att atg	1824
Arg Leu Gln Glu Leu Asp Lys Ser Asn Pro Ile Leu Leu Arg Ile Met	
595 600 605	
aat gac cag ctg atg tat ctg gaa cgt gca ttc att gat cct tta ggc	1872
Asn Asp Gln Leu Met Tyr Leu Glu Arg Ala Phe Ile Asp Pro Leu Gly	
610 615 620	
tta cca gga agg cct ttc tac agg cat acc atc tat gct cca agc agc	1920
Leu Pro Gly Arg Pro Phe Tyr Arg His Thr Ile Tyr Ala Pro Ser Ser	
625 630 635 640	
cac aac aag tat gca gga gaa tca ttc cct ggg att tat gat gcc ctt	1968
His Asn Lys Tyr Ala Gly Glu Ser Phe Pro Gly Ile Tyr Asp Ala Leu	
645 650 655	
ttt gat ata agt agc aaa gtc aat gct tct aag gcc tgg aac gaa gtg	2016
Phe Asp Ile Ser Ser Lys Val Asn Ala Ser Lys Ala Trp Asn Glu Val	
660 665 670	

aag aga cag att tct att gca acc ttt aca gtg caa gct gca gca gag 2064
Lys Arg Gln Ile Ser Ile Ala Thr Phe Thr Val Gln Ala Ala Ala Glu
675 680 685
act ctg agg gaa gta gct 2082
Thr Leu Arg Gln Val Ala
690

<210> 10
<211> 694
<212> PRT
<213> Mus musculus

<400> 10
Met Lys Lys Glu Phe Leu His Glu Leu Lys Ala Glu Asn Ile Lys Lys
1 5 10 15
Phe Leu Tyr Asn Phe Thr Arg Thr Pro His Leu Ala Gly Thr Gln Asn
20 25 30
Asn Phe Glu Leu Ala Lys Gln Ile His Asp Gln Trp Lys Glu Phe Gly
35 40 45
Leu Asp Leu Val Glu Leu Ser His Tyr Asp Val Leu Leu Ser Tyr Pro
50 55 60
Asn Lys Thr His Pro Asn Tyr Ile Ser Ile Ile Asn Glu Asp Gly Asn
65 70 75 80
Glu Ile Phe Lys Thr Ser Leu Ser Glu Gln Pro Pro Gly Tyr Glu
85 90 95
Asn Ile Ser Asp Val Val Pro Pro Tyr Ser Ala Phe Ser Pro Gln Gly
100 105 110
Thr Pro Glu Gly Asp Leu Val Tyr Val Asn Tyr Ala Arg Thr Glu Asp
115 120 125
Phe Phe Lys Leu Glu Arg Glu Met Lys Ile Ser Cys Ser Gly Lys Ile
130 135 140
Val Ile Ala Arg Tyr Gly Lys Val Phe Arg Gly Asn Met Val Lys Asn
145 150 155 160
Ala Gln Leu Ala Gly Ala Lys Gly Met Ile Leu Tyr Ser Asp Pro Ala
165 170 175
Asp Tyr Phe Val Pro Ala Val Lys Ser Tyr Pro Asp Gly Trp Asn Leu
180 185 190
Pro Gly Gly Gly Val Gln Arg Gly Asn Val Leu Asn Leu Asn Gly Ala
195 200 205
Gly Asp Pro Leu Thr Pro Gly Tyr Pro Ala Asn Glu His Ala Tyr Arg
210 215 220
His Glu Leu Thr Asn Ala Val Gly Leu Pro Ser Ile Pro Val His Pro
225 230 235 240
Ile Gly Tyr Asp Asp Ala Gln Lys Leu Leu Glu His Met Gly Gly Pro
245 250 255
Ala Pro Pro Asp Ser Ser Trp Lys Gly Gly Leu Lys Val Pro Tyr Asn
260 265 270
Val Gly Pro Gly Phe Ala Gly Asn Phe Ser Thr Gln Lys Val Lys Met
275 280 285
His Ile His Ser Tyr Thr Lys Val Thr Arg Ile Tyr Asn Val Ile Gly
290 295 300
Thr Leu Lys Gly Ala Leu Glu Pro Asp Arg Tyr Val Ile Leu Gly Gly
305 310 315 320
His Arg Asp Ala Trp Val Phe Gly Gly Ile Asp Pro Gln Ser Gly Ala
325 330 335
Ala Val Val His Glu Ile Val Arg Ser Phe Gly Thr Leu Lys Lys Lys

<400> 11
 cag tac atc aaa gct aac tcc aaa ttc atc ggt atc acc gag ctg 45
 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
 1 5 10 15

<210> 12
 <211> 15
 <212> PRT
 <213> Clostridium tetani

<400> 12
 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
 1 5 10 15

<210> 13
 <211> 63
 <212> DNA
 <213> Clostridium tetani

<220>
 <221> CDS
 <222> (1)..(63)

<400> 13
 ttc aac aac ttc acc gta agc ttc tgg ctg cgt gtt ccg aaa gtt agc 48
 Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
 1 5 10 15
 gct agc cac ctg gaa 63
 Ala Ser His Leu Glu
 20

<210> 14
 <211> 21
 <212> PRT
 <213> Clostridium tetani

<400> 14
 Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
 1 5 10 15
 Ala Ser His Leu Glu
 20

<210> 15
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion of
 tetanus toxoid epitope and PSM

<400> 15

Gln Glu Arg Gly Val Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly
1 5 10 15
Ile Thr Glu Leu Arg Val Asp Cys Thr
20 25

<210> 16

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion of
tetanus toxoid epitope and PSM

<400> 16

Ala Val Val Leu Arg Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly
1 5 10 15
Ile Thr Glu Leu Glu Met Lys Thr Tyr
20 25

<210> 17

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion of
tetanus toxoid epitope and PSM

<400> 17

Met Phe Leu Glu Arg Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly
1 5 10 15
Ile Thr Glu Leu His Val Ile Tyr Ala
20 25

<210> 18

<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion of
tetanus toxoid epitope and PSM

<400> 18

Asn Ser Arg Leu Leu Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg
1 5 10 15
Val Pro Lys Val Ser Ala Ser His Leu Glu Val Asp Cys Thr Pro
20 25 30

<210> 19
 <211> 31
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion of
 tetanus toxoid epitope and PSM

<400> 19
 Val Val Leu Arg Lys Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg
 1 5 10 15
 Val Pro Lys Val Ser Ala Ser His Leu Glu Ser Phe Asp Ser Leu
 20 25 30

<210> 20
 <211> 31
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion of
 tetanus toxoid epitope and PSM

<400> 20
 Leu Met Phe Leu Glu Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg
 1 5 10 15
 Val Pro Lys Val Ser Ala Ser His Leu Glu Pro Ser Ser His Asn
 20 25 30

<210> 21
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Artificial His
 tag

<220>
 <221> CDS
 <222> (1)..(18)

<400> 21
 cat cat cat cat cat cat
 His His His His His His
 1 5

18

<210> 22
 <211> 6

<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial His
tag

<400> 22

His His His His His His
1 5

<210> 23

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial His
tag

<220>

<221> CDS

<222> (1)..(42)

<400> 23

atg aaa cac caa cac caa cat caa cat caa cat caa cat caa
Met Lys His Gln His Gln His Gln His Gln His Gln His Gln
1 5 10

42

<210> 24

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial His
tag

<400> 24

Met Lys His Gln His Gln His Gln His Gln His Gln His Gln
1 5 10

<210> 25

<211> 69

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(69)

<400> 25

atg gat gca atg aag aga ggg ctc tgc tgt gtg ctg ctg ctg tgt gga 48
 Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1 5 10 15

gca gtc ttc gtt tgc ccc agc 69
 Ala Val Phe Val Ser Pro Ser
 20

<210> 26
 <211> 23
 <212> PRT
 <213> Mus musculus

<400> 26
 Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1 5 10 15
 Ala Val Phe Val Ser Pro Ser
 20

<210> 27
 <211> 33
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(33)

<400> 27 33
 gaa caa aaa ctc atc tca gaa gag gat ctg aat
 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
 1 5 10

<210> 28
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 28
 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
 1 5 10

<210> 29
 <211> 75
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(75)

<400> 29 48
 atg aag gat tcc tgc atc act gtg atg gcc atg gcg ctg ctg tct ggg

Met Lys Asp Ser Cys Ile Thr Val Met Ala Met Ala Leu Leu Ser Gly
 1 5 10 15
 ttc ttt ttc ttc gcg ccg gcc tcg agc 75
 Phe Phe Phe Phe Ala Pro Ala Ser Ser
 20 25

<210> 30
 <211> 25
 <212> PRT
 <213> Homo sapiens

<400> 30
 Met Lys Asp Ser Cys Ile Thr Val Met Ala Met Ala Leu Leu Ser Gly
 1 5 10 15
 Phe Phe Phe Phe Ala Pro Ala Ser Ser
 20 25

<210> 31
 <211> 60
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(60)

<400> 31
 atg aga agg atg ctt ctg cac ttg agt gtt ctg act ctc agc tgt gtc 48
 Met Arg Arg Met Leu Leu His Leu Ser Val Leu Thr Leu Ser Cys Val
 1 5 10 15
 tgg gcc act gcc 60
 Trp Ala Thr Ala
 20

<210> 32
 <211> 20
 <212> PRT
 <213> Mus musculus

<400> 32
 Met Arg Arg Met Leu Leu His Leu Ser Val Leu Thr Leu Ser Cys Val
 1 5 10 15
 Trp Ala Thr Ala
 20

<210> 33
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 33
 Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala

1 5 10 15
 Pro Asp Thr Arg
 20

<210> 34
 <211> 244
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fig. 5B - Various FGF8 isoforms

<400> 34
 Met Gly Ser Pro Arg Ser Ala Leu Ser Cys Leu Leu Leu His Leu Leu
 1 5 10 15
 Val Leu Cys Leu Gln Ala Gln Glu Gly Pro Gly Arg Gly Pro Ala Leu
 20 25 30
 Gly Arg Glu Leu Ala Ser Leu Phe Arg Ala Gly Arg Glu Pro Gln Gly
 35 40 45
 Val Ser Gln Gln Val Thr Val Gln Ser Ser Pro Asn Phe Thr Gln His
 50 55 60
 Val Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg Arg Leu Ile
 65 70 75 80
 Arg Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His Val Gln Val
 85 90 95
 Leu Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly Asp Pro Phe
 100 105 110
 Ala Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg Val Arg Val
 115 120 125
 Arg Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys Lys Gly Lys
 130 135 140
 Leu Ile Ala Lys Ser Asn Gly Lys Gly Lys Asp Cys Val Phe Thr Glu
 145 150 155 160
 Ile Val Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala Lys Tyr Glu
 165 170 175
 Gly Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg Lys Gly Ser
 180 185 190
 Lys Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys Arg Leu Pro
 195 200 205
 Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu Phe Leu Asn
 210 215 220
 Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg Thr Trp Ala
 225 230 235 240
 Pro Glu Pro Arg

<210> 35
 <211> 215
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(215)
 <223> Fig. 6 - Wild Type (WT) FGF8b

<400> 35

Met Gly Ser Pro Arg Ser Ala Leu Ser Cys Leu Leu Leu His Leu Leu
1 5 10 15
Val Leu Cys Leu Gln Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe
20 25 30
Thr Gln His Val Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg
35 40 45
Arg Leu Ile Arg Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His
50 55 60
Val Gln Val Leu Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly
65 70 75 80
Asp Pro Phe Ala Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg
85 90 95
Val Arg Val Arg Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys
100 105 110
Lys Gly Lys Leu Ile Ala Lys Ser Asn Gly Lys Gly Lys Asp Cys Val
115 120 125
Phe Thr Glu Ile Gly Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala
130 135 140
Lys Tyr Glu Gly Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg
145 150 155 160
Lys Gly Ser Lys Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys
165 170 175
Arg Leu Pro Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu
180 185 190
Phe Leu Asn Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg
195 200 205
Thr Trp Ala Pro Glu Pro Arg
210 215

<210> 36

<211> 195

<212> PRT

<213> Artificial Sequence

<220>

<223> Fig. 6 - F30N: Variant of FGF8b with P30 epitope in the N-terminal

<400> 36

Met Ala Gln Val Thr Val Phe Asn Asn Phe Thr Val Ser Phe Trp Leu
1 5 10 15
Arg Val Pro Lys Val Ser Ala Ser His Leu Glu Arg Arg Leu Ile Arg
20 25 30
Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His Val Gln Val Leu
35 40 45
Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly Asp Pro Phe Ala
50 55 60
Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg Val Arg Val Arg
65 70 75 80
Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys Lys Gly Lys Leu
85 90 95
Ile Ala Lys Ser Asn Gly Lys Gly Lys Asp Cys Val Phe Thr Glu Ile
100 105 110
Gly Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala Lys Tyr Glu Gly
115 120 125
Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg Lys Gly Ser Lys

130		135		140
Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys Arg Leu Pro Arg				
145		150		155
Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu Phe Leu Asn Tyr				
	165		170	175
Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg Thr Trp Ala Pro				
	180		185	190
Glu Pro Arg				
195				

<210> 37
 <211> 208
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Fig. 6 - F2I: Internal variant of FGF8b constructed by replacing external loops in the FGF2 structure with P2 epitope

<400> 37	
Met Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe Thr Gln His Val	
1	5 10 15
Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg Arg Leu Ile Arg	
	20 25 30
Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His Val Gln Val Leu	
	35 40 45
Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly Asp Pro Phe Ala	
	50 55 60
Lys Leu Ile Val Glu Thr Asp Gln Tyr Ile Lys Ala Asn Ser Lys Phe	
65	70 75 80
Ile Gly Ile Thr Glu Leu Gly Ser Arg Val Arg Val Arg Gly Ala Glu	
	85 90 95
Thr Gly Leu Tyr Ile Cys Met Asn Lys Lys Gly Lys Leu Ile Ala Lys	
	100 105 110
Ser Asn Gly Lys Gly Lys Asp Cys Val Phe Thr Glu Ile Gly Leu Glu	
	115 120 125
Asn Asn Tyr Thr Ala Leu Gln Asn Ala Lys Tyr Glu Gly Trp Tyr Met	
	130 135 140
Ala Phe Thr Arg Lys Gly Arg Pro Arg Lys Gly Ser Lys Thr Arg Gln	
145	150 155 160
His Gln Arg Glu Val His Phe Met Lys Arg Leu Pro Arg Gly His His	
	165 170 175
Thr Thr Glu Gln Ser Leu Arg Phe Glu Phe Leu Asn Tyr Pro Pro Phe	
	180 185 190
Thr Arg Ser Leu Arg Gly Ser Gln Arg Thr Trp Ala Pro Glu Pro Arg	
	195 200 205

<210> 38
 <211> 213
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Fig. 6 - F30I: Internal variant of FGF8b constructed by replacing

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external loops in the FGF2 structure with P30 epitope

<400> 38

```

Met Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe Thr Gln His Val
1          5          10          15
Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg Arg Leu Ile Arg
          20          25          30
Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His Val Gln Val Leu
          35          40          45
Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly Asp Pro Phe Ala
          50          55          60
Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg Val Arg Val Arg
65          70          75          80
Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys Lys Gly Lys Leu
          85          90          95
Ile Ala Lys Ser Asn Gly Phe Asn Asn Phe Thr Val Ser Phe Trp Leu
          100         105         110
Arg Val Pro Lys Val Ser Ala Ser His Leu Glu Asp Cys Val Phe Thr
          115         120         125
Glu Ile Gly Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala Lys Tyr
          130         135         140
Glu Gly Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg Lys Gly
145         150         155         160
Ser Lys Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys Arg Leu
          165         170         175
Pro Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu Phe Leu
          180         185         190
Asn Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg Thr Trp
          195         200         205
Ala Pro Glu Pro Arg
          210

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<210> 39

<211> 199

<212> PRT

<213> Artificial Sequence

<220>

<223> Fig. 6 -F2C: Variant of FGF8b with P2 epitope in the C-terminal

<400> 39

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Met Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe Thr Gln His Val
1          5          10          15
Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg Arg Leu Ile Arg
          20          25          30
Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His Val Gln Val Leu
          35          40          45
Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly Asp Pro Phe Ala
          50          55          60
Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg Val Arg Val Arg
65          70          75          80
Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys Lys Gly Lys Leu
          85          90          95
Ile Ala Lys Ser Asn Gly Lys Gly Lys Asp Cys Val Phe Thr Glu Ile
          100         105         110

```

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Gly Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala Lys Tyr Glu Gly
 115 120 125
 Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg Lys Gly Ser Lys
 130 135 140
 Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys Arg Leu Pro Arg
 145 150 155 160
 Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu Phe Leu Asn Tyr
 165 170 175
 Pro Pro Phe Thr Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile
 180 185 190
 Thr Glu Leu Pro Glu Pro Arg
 195

<210> 40
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A preferred pan DR epitope (PADRE) peptide has this sequence
 <400> 40

Ala Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala
 1 5 10

<210> 41
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FGF8b specific peptide
 <400> 41

Gln Val Thr Val Gln Ser Ser Pro Asn Phe Thr
 1 5 10